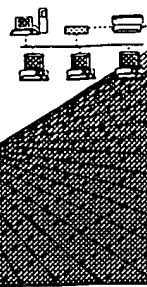BIOT. NOLOGY
S. .EMS
BRANCH

#13

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/574,735_

Source: _1600_

Date Processed by STIC: _7-20-01_

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
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TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

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Checker Version 3.0 can be down loaded from the USPTO website at the following address:
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1600

RAW SEQUENCE LISTING   DATE: 07/20/2001
PATENT APPLICATION: US/09/574,735   TIME: 13:18:29

Input Set : **A:\cpg.txt**
Output Set: **N:\CRF3\07202001\I574735.raw**

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 3 <110> APPLICANT: De Veylder, Lieven
 4        Beeckman, Tom
 5        Inz,, Dirk
 6        Van Camp, Wim
 7        Krols, Luc
10 <120> TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
13 <130> FILE REFERENCE: 2283/301
16 <140> CURRENT APPLICATION NUMBER: US 09/574,735
17 <141> CURRENT FILING DATE: 2000-05-18
20 <160> NUMBER OF SEQ ID NOS: 48
23 <170> SOFTWARE: PatentIn version 3.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 932
28 <212> TYPE: DNA
29 <213> ORGANISM: Arabidopsis thaliana
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (86)..(712)
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37 ctggaaggtg acgtcgtagg agatt atg gcg gcg gtt agg aga aga gaa cga       112
38                           Met Ala Ala Val Arg Arg Arg Glu Arg
39                           1               5
40 gat gtg gtt gaa gag aat gga gtt acg acg acg acg gtg aaa cga agg      160
41 Asp Val Val Glu Glu Asn Gly Val Thr Thr Thr Thr Val Lys Arg Arg
42 10              15                  20                  25
43 aag atg gag gag gaa gtg gat tta gtg gaa tct agg ata att ctg tct      208
44 Lys Met Glu Glu Glu Val Asp Leu Val Glu Ser Arg Ile Ile Leu Ser
45             30                  35                  40
46 ccg tgt gta cag gcg acg aat cgc ggt gga att gtg gcg aga aat tca      256
47 Pro Cys Val Gln Ala Thr Asn Arg Gly Gly Ile Val Ala Arg Asn Ser
48             45                  50                  55
49 gca gga gcg tcg gag acg agt gtt gtt ata gta cga cgg cga gat tct      304
50 Ala Gly Ala Ser Glu Thr Ser Val Val Ile Val Arg Arg Arg Asp Ser
51         60                  65                  70
52 cct ccg gtt gaa gaa cag tgt caa atc gaa gaa gaa gat tcg tcg gtt      352
53 Pro Pro Val Glu Glu Gln Cys Gln Ile Glu Glu Glu Asp Ser Ser Val
54     75                  80                  85
55 tcg tgt tgt tct aca tcg gaa gag aaa tcg aaa cgg aga atc gaa ttt      400
56 Ser Cys Cys Ser Thr Ser Glu Glu Lys Ser Lys Arg Arg Ile Glu Phe
57 90                  95                  100                 105
58 gta gat ctt gag gaa aat aac ggt gac gat cgt gaa aca gaa acg tcg      448
59 Val Asp Leu Glu Glu Asn Asn Gly Asp Asp Arg Glu Thr Glu Thr Ser
60                 110                 115                 120
61 tgg att tac gat gat ttg aat aag agt gag gaa tcg atg aac atg gat      496
62 Trp Ile Tyr Asp Asp Leu Asn Lys Ser Glu Glu Ser Met Asn Met Asp
63                 125                 130                 135
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64 tct tct tcg gtg gct gtt gaa gat gta gag tct cgc cgc agg tta agg       544
65 Ser Ser Ser Val Ala Val Glu Asp Val Glu Ser Arg Arg Arg Leu Arg
66         140             145             150
67 aag agt ctc cat gag acg gtg aag gaa gct gag tta gaa gat ttt ttt       592
68 Lys Ser Leu His Glu Thr Val Lys Glu Ala Glu Leu Glu Asp Phe Phe
69         155             160             165
70 cag gtg gcg gag aaa gat ctt cgg aat aag ttg ttg gaa tgt tct atg       640
71 Gln Val Ala Glu Lys Asp Leu Arg Asn Lys Leu Leu Glu Cys Ser Met
72 170             175             180             185
73 aag tat aac ttc gat ttc gag aaa gat gag cca ctt ggt gga gga aga       688
74 Lys Tyr Asn Phe Asp Phe Glu Lys Asp Glu Pro Leu Gly Gly Gly Arg
75             190             195             200
76 tac gag tgg gtt aaa ttg aat cca tgaagaagac gatgatgata atgatgatca      742
77 Tyr Glu Trp Val Lys Leu Asn Pro
78             205
79 ttgttttcac caaagtactt attatttttc ttctgtaata atctttgctt tgattttct      802
80 tttaacaaaa tccaaatgta gatatctttc tctcgaataa tcaataacat gtaattcaac      862
81 ttttgtttgt acttccttga ggtaattaat tagattcgtg tttttctcga ttaataaact      922
82 ataagtttat                                                            932
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86 <211> LENGTH: 209
87 <212> TYPE: PRT
88 <213> ORGANISM: Arabidopsis thaliana
90 <400> SEQUENCE: 2
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93 Val Thr Thr Thr Thr Val Lys Arg Arg Lys Met Glu Glu Glu Val Asp
94             20              25              30
95 Leu Val Glu Ser Arg Ile Ile Leu Ser Pro Cys Val Gln Ala Thr Asn
96         35              40              45
97 Arg Gly Gly Ile Val Ala Arg Asn Ser Ala Gly Ala Ser Glu Thr Ser
98     50              55              60
99 Val Val Ile Val Arg Arg Arg Asp Ser Pro Pro Val Glu Glu Gln Cys
100 65              70              75              80
101 Gln Ile Glu Glu Glu Asp Ser Ser Val Ser Cys Cys Ser Thr Ser Glu
102             85              90              95
103 Glu Lys Ser Lys Arg Arg Ile Glu Phe Val Asp Leu Glu Glu Asn Asn
104         100             105             110
105 Gly Asp Asp Arg Glu Thr Glu Thr Ser Trp Ile Tyr Asp Asp Leu Asn
106     115             120             125
107 Lys Ser Glu Glu Ser Met Asn Met Asp Ser Ser Ser Val Ala Val Glu
108     130             135             140
109 Asp Val Glu Ser Arg Arg Arg Leu Arg Lys Ser Leu His Glu Thr Val
110 145             150             155             160
111 Lys Glu Ala Glu Leu Glu Asp Phe Phe Gln Val Ala Glu Lys Asp Leu
112             165             170             175
113 Arg Asn Lys Leu Leu Glu Cys Ser Met Lys Tyr Asn Phe Asp Phe Glu
114         180             185             190
115 Lys Asp Glu Pro Leu Gly Gly Gly Arg Tyr Glu Trp Val Lys Leu Asn
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/574,735

DATE: 07/20/2001
TIME: 13:18:29.

Input Set : A:\cpg.txt
Output Set: N:\CRF3\07202001\I574735.raw

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123 <212> TYPE: DNA
124 <213> ORGANISM: Arabidopsis thaliana
126 <220> FEATURE:
127 <221> NAME/KEY: CDS
128 <222> LOCATION: (11)..(658)
130 <400> SEQUENCE: 3
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133             1           5                     10
134 tct aaa gca aca gct cca agt cca ggt gtt cga acc aga gcc gct aaa      97
135 Ser Lys Ala Thr Ala Pro Ser Pro Gly Val Arg Thr Arg Ala Ala Lys
136      15                20                  25
137 acc cta gcc ttg aag cgg ctt aat tcc tcc gcc gct gat tca gct cta     145
138 Thr Leu Ala Leu Lys Arg Leu Asn Ser Ser Ala Ala Asp Ser Ala Leu
139 30                35                  40                  45
140 cct aac gac tct tct tgc tat ctt cag ctc cgt agc cgc cgt ctc gag     193
141 Pro Asn Asp Ser Ser Cys Tyr Leu Gln Leu Arg Ser Arg Arg Leu Glu
142                50                  55                  60
143 aaa ccc tct tcg ctg att gaa ccg aaa cag ccg ccg aga gtt cac aga     241
144 Lys Pro Ser Ser Leu Ile Glu Pro Lys Gln Pro Pro Arg Val His Arg
145            65                  70                  75
146 tcg gga att aaa gag tct ggt tcc agg tct cgc gtt gac tcg gtt aac     289
147 Ser Gly Ile Lys Glu Ser Gly Ser Arg Ser Arg Val Asp Ser Val Asn
148         80                  85                  90
149 tcg gtt cct gta gct cag agc tct aat gaa gat gaa tgt ttt gac aat     337
150 Ser Val Pro Val Ala Gln Ser Ser Asn Glu Asp Glu Cys Phe Asp Asn
151      95                  100                 105
152 ttc gtg agt gtc caa gtt tct tgt ggt gaa aac agt ctc ggt ttt gaa     385
153 Phe Val Ser Val Gln Val Ser Cys Gly Glu Asn Ser Leu Gly Phe Glu
154 110                 115                 120                 125
155 tca aga cac agc aca agg gag agc acg cct tgt aac ttt gtt gag gat     433
156 Ser Arg His Ser Thr Arg Glu Ser Thr Pro Cys Asn Phe Val Glu Asp
157                130                 135                 140
158 atg gag atc atg gtt aca cca ggg tct agc acg agg tcg atg tgc aga     481
159 Met Glu Ile Met Val Thr Pro Gly Ser Ser Thr Arg Ser Met Cys Arg
160                145                 150                 155
161 gca acc aaa gag tac aca agg gaa caa gat aac gtg atc ccg acc act     529
162 Ala Thr Lys Glu Tyr Thr Arg Glu Gln Asp Asn Val Ile Pro Thr Thr
163            160                 165                 170
164 agt gaa atg gag gag ttc ttt gca tat gca gag cag cag caa cag agg     577
165 Ser Glu Met Glu Glu Phe Phe Ala Tyr Ala Glu Gln Gln Gln Gln Arg
166      175                 180                 185
167 cta ttc atg gag aag tac aac ttc gac att gtg aat gat atc ccc ctc     625
168 Leu Phe Met Glu Lys Tyr Asn Phe Asp Ile Val Asn Asp Ile Pro Leu
169 190                 195                 200                 205
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Input Set : A:\cpg.txt
Output Set: N:\CRF3\07202001\I574735.raw

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170 agc gga cgt tac gaa tgg gtg caa gtc aaa cca tgaagttcaa aaggaaacag   678
171 Ser Gly Arg Tyr Glu Trp Val Gln Val Lys Pro
172                 210                 215
173 ctccaaaaga catggtgtga agttagagaa tgtgatggag ttaacagact aaccaaacat   738
174 cagaaatcgt gtaatcttaa gtaataatgt ggttagagaa caagtttgag agtagcttag   798
175 ggaccttaaa acctcacacc atttgtaata ctaatcttct tcagatgctt agtgaaattt   858
176 tctcatctgt ttctttc                                                  875
179 <210> SEQ ID NO: 4
180 <211> LENGTH: 216
181 <212> TYPE: PRT
182 <213> ORGANISM: Arabidopsis thaliana
184 <400> SEQUENCE: 4
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187 Thr Ala Pro Ser Pro Gly Val Arg Thr Arg Ala Ala Lys Thr Leu Ala
188             20                  25                  30
189 Leu Lys Arg Leu Asn Ser Ser Ala Ala Asp Ser Ala Leu Pro Asn Asp
190         35                  40                  45
191 Ser Ser Cys Tyr Leu Gln Leu Arg Ser Arg Arg Leu Glu Lys Pro Ser
192     50                  55                  60
193 Ser Leu Ile Glu Pro Lys Gln Pro Pro Arg Val His Arg Ser Gly Ile
194 65                  70                  75                  80
195 Lys Glu Ser Gly Ser Arg Ser Arg Val Asp Ser Val Asn Ser Val Pro
196             85                  90                  95
197 Val Ala Gln Ser Ser Asn Glu Asp Glu Cys Phe Asp Asn Phe Val Ser
198             100                 105                 110
199 Val Gln Val Ser Cys Gly Glu Asn Ser Leu Gly Phe Glu Ser Arg His
200         115                 120                 125
201 Ser Thr Arg Glu Ser Thr Pro Cys Asn Phe Val Glu Asp Met Glu Ile
202     130                 135                 140
203 Met Val Thr Pro Gly Ser Ser Thr Arg Ser Met Cys Arg Ala Thr Lys
204 145                 150                 155                 160
205 Glu Tyr Thr Arg Glu Gln Asp Asn Val Ile Pro Thr Thr Ser Glu Met
206             165                 170                 175
207 Glu Glu Phe Phe Ala Tyr Ala Glu Gln Gln Gln Gln Arg Leu Phe Met
208             180                 185                 190
209 Glu Lys Tyr Asn Phe Asp Ile Val Asn Asp Ile Pro Leu Ser Gly Arg
210         195                 200                 205
211 Tyr Glu Trp Val Gln Val Lys Pro
212     210                 215
215 <210> SEQ ID NO: 5
216 <211> LENGTH: 1193
217 <212> TYPE: DNA
218 <213> ORGANISM: Arabidopsis thaliana
220 <220> FEATURE:
221 <221> NAME/KEY: CDS
222 <222> LOCATION: (92)..(763)
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226 cttcaaattc ttcccctgtt tttcaacttc a atg ggg aag tac atg aag aaa      112
227                                      Met Gly Lys Tyr Met Lys Lys
228                                       1                 5
229 ctc aaa tcc aaa tca gaa tct cct tca ccc aat tca aca cca aca cca     160
230 Leu Lys Ser Lys Ser Glu Ser Pro Ser Pro Asn Ser Thr Pro Thr Pro
231        10                  15                  20
232 tca cca tca cca tca cca aca cca atc acc acc aat tca cca cca cca     208
233 Ser Pro Ser Pro Ser Pro Thr Pro Ile Thr Thr Asn Ser Pro Pro Pro
234        25                  30                  35
235 aca aca ccc aat tcc tct gat ggt gtt cga act cgt gct aga acc cta    256
236 Thr Thr Pro Asn Ser Ser Asp Gly Val Arg Thr Arg Ala Arg Thr Leu
237 40                  45                  50                  55
238 gct ttg gag aat tcc aac aat cag aat cag aat ctt tct gtt tct tct    304
239 Ala Leu Glu Asn Ser Asn Asn Gln Asn Gln Asn Leu Ser Val Ser Ser
240                  60                  65                  70
241 gat tct tac ctt cag ctg agg aac cgt cgc ctt aag aga ccc cta att    352
242 Asp Ser Tyr Leu Gln Leu Arg Asn Arg Arg Leu Lys Arg Pro Leu Ile
243                  75                  80                  85
244 agg caa cat tcc gct aag agg aat aag ggg cat gat gga aac cct aaa     400
245 Arg Gln His Ser Ala Lys Arg Asn Lys Gly His Asp Gly Asn Pro Lys
246                  90                  95                  100
247 tcc cca att ggg gat tca att gct gaa gag aaa act gtt cag aag agt     448
248 Ser Pro Ile Gly Asp Ser Ile Ala Glu Glu Lys Thr Val Gln Lys Ser
249        105                 110                 115
250 cct gag cct gaa aat gct gaa ttc aag gag aat gct gag gat act gag     496
251 Pro Glu Pro Glu Asn Ala Glu Phe Lys Glu Asn Ala Glu Asp Thr Glu
252 120                 125                 130                 135
253 aga agc gct agg gaa act aca ccc gtc cat ttg ata atg cga gca gac    544
254 Arg Ser Ala Arg Glu Thr Thr Pro Val His Leu Ile Met Arg Ala Asp
255                 140                 145                 150
256 gtt ctc agg cct cct agg cca att acc agg cgt act ttt cca act gaa    592
257 Val Leu Arg Pro Pro Arg Pro Ile Thr Arg Arg Thr Phe Pro Thr Glu
258                 155                 160                 165
259 gct aat ccc aaa acg gag cag cca act atc cca att tca cgc gaa ttt    640
260 Ala Asn Pro Lys Thr Glu Gln Pro Thr Ile Pro Ile Ser Arg Glu Phe
261        170                 175                 180
262 gag gaa ttc tgt gct aaa cat gaa gcc gag cag caa agg gag ttc atg    688
263 Glu Glu Phe Cys Ala Lys His Glu Ala Glu Gln Gln Arg Glu Phe Met
264        185                 190                 195
265 gag aag tac aac ttt gat cct gtg aca gag cag cca ctc cca ggg cgt    736
266 Glu Lys Tyr Asn Phe Asp Pro Val Thr Glu Gln Pro Leu Pro Gly Arg
267 200                 205                 210                 215
268 tac gaa tgg gaa aaa gtg tcg ccc tag aaggcaggct agtattaagt          783
269 Tyr Glu Trp Glu Lys Val Ser Pro
270                 220
271 gttccatcaa tacatcttta aagtagcagc agggttagaa tttgttgaaa agggtggtgg  843
272 tgctatttcc attttccatc actttctatt tacttgtaaa gaaagtagga ctttcaacat  903
273 atgtagacta atgatctgta actttacaga ggtgttgatt acacaacaat acaaagtcct  963
274 ttgtctagca gatcattaaa gaagggtttg agggaataag ggtctctagt tgtagggttt 1023
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/574,735**

DATE: 07/20/2001
TIME: 13:18:30

Input Set : **A:\cpg.txt**
Output Set: **N:\CRF3\07202001\I574735.raw**

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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/574,735**

DATE: 07/20/2001
TIME: 13:18:30

Input Set : **A:\cpg.txt**
Output Set: **N:\CRF3\07202001\I574735.raw**

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L:593 M:283 W: Missing Blank Line separator, <220> field identifier
L:598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:610 M:283 W: Missing Blank Line separator, <220> field identifier
L:615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:629 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:641 M:283 W: Missing Blank Line separator, <220> field identifier
L:644 M:283 W: Missing Blank Line separator, <220> field identifier
L:649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
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